#6

FIG. 1A

```
  1  CCCACGCGTCCGGGGAGCTTGCACTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC   60

 61  CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTCATAAATATAATTTGCTC  120

121  TTTCACTTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA  180

181  GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG  240

241  CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC  300

301  TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT  360

361  AAGGGAAAACTAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT  420

421  GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAACTGAGCATGGAGAGAAAAATT  480

481  TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA  540
  1                                      M  E  P  N  G  T  F  S  N    9

541  TAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTTTTCCCAATTGTATA  600
 10   N  N  S  R  N  C  T  I  E  N  F  K  R  E  F  F  P  I  V  Y   29

601  TCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCCTGCA  660
 30   L  I  I  F  F  W  G  V  L  G  N  G  L  S  I  Y  V  F  L  Q   49

661  GCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCT  720
 50   P  Y  K  K  S  T  S  V  N  V  F  M  L  N  L  A  I  S  D  L   69

721  CCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT  780
 70   L  F  I  S  T  L  P  F  R  A  D  Y  Y  L  R  G  S  N  W  I   89

781  ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAG  840
 90   F  G  D  L  A  C  R  I  M  S  Y  S  L  Y  V  N  M  Y  S  S  109

841  TATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCG  900
110   I  Y  F  L  T  V  L  S  V  V  R  F  L  A  M  V  H  P  F  R  129
```

FIG. 1B

```
901  GCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCT   960
130   L  L  H  V  T  S  I  R  S  A  W  I  L  C  G  I  I  W  I  L   149

961  TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCAC  1020
150   I  M  A  S  S  I  M  L  L  D  S  G  S  E  Q  N  G  S  V  T   169

1021 ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGC  1080
170   S  C  L  E  L  N  L  Y  K  I  A  K  L  Q  T  M  N  Y  I  A   189

1081 CTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCAT  1140
190   L  V  V  G  C  L  L  P  F  F  T  L  S  I  C  Y  L  L  I  I   209

1141 TCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGC  1200
210   R  V  L  L  K  V  E  V  P  E  S  G  L  R  V  S  H  R  K  A   229

1201 ACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCCTGCCCTATCACAC  1260
230   L  T  T  I  I  I  T  L  I  I  F  F  L  C  F  L  P  Y  H  T   249

1261 ACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAA  1320
250   L  R  T  V  H  L  T  T  W  K  V  G  L  C  K  D  R  L  H  K   269

1321 AGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTA  1380
270   A  L  V  I  T  L  A  L  A  A  A  N  A  C  F  N  P  L  L  Y   289

1381 TTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC  1440
290   Y  F  A  G  E  N  F  K  D  R  L  K  S  A  L  R  K  G  H  P   309

1441 ACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAG  1500
310   Q  K  A  K  T  K  C  V  F  P  V  S  V  W  L  R  K  E  T  R   329

1501 AGTATAAGGAGCTCTTAGATGAGACCTGTTCTTGTATCCTTGTGTCCATCTTCATTCACT  1560
330   V  *                                                         331

1561 CATAGTCTCCAAATGACTTTGTATTTACATCACTCCCAACAAATGTTGATTCTTAATATT  1620

1621 TAGTTGACCATTACTTTTGTTAATAAGACCTACTTCAAAAATTTTATTCAGTGTAAAAAA  1680

1681 AAAAAAAAAAAAAAAAAAAAAAAAAAAA  1708
```

FIG. 2A

```
                      1                                                50
HGPRBMY11      (1)    -----MSLQPSISVSEMEPNG-----------TFSNNNSRNCTIEN--FK
HGPRBMY11v1    (1)    MERKFMSLQPSISVSEMEPNG-----------TFSNNNSRNCTIEN--FK
P2Y5_CHICK     (1)    ------------------------------------MVSSNCSTEDS-FK
P2YR_CHICK     (1)    MTEALISAALNGTQPELLAGG-----------WAAGNASTKCSLTKTGFQ
P2YR_MELGA     (1)    MTEALISAALNGTQPELLAGG-----------WAAGNASTKCSLTKTGFQ
P2YR_RAT       (1)    MTEVPWSAVPNGTDAAFLAGLGSLWGNSTIASTAAVSSSFRCALIKTGFQ
Q9Y271         (1)    ----------------MDETG------------NLTVSSATCHDTIDDFR
GPRH_HUMAN     (1)    -----------MNGLEVAPPG---------LITNFSLATAEQCGQETPLE

                      51                                              100
HGPRBMY11      (22)   REFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLF
HGPRBMY11v1    (38)   REFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISDLLF
P2Y5_CHICK     (14)   YTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMINLAMSDLLF
P2YR_CHICK     (40)   FYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLY
P2YR_MELGA     (40)   FYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLY
P2YR_RAT       (51)   FYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLY
Q9Y271         (23)   NQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVADLLC
GPRH_HUMAN     (31)   NMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSC

                      101                                             150
HGPRBMY11      (72)   ISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRF
HGPRBMY11v1    (88)   ISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRF
P2Y5_CHICK     (64)   VFTLPFRIYYEVVRN-WPFGDVLCKISVTLFYTNMYGSILFLTCISVDRF
P2YR_CHICK     (90)   VLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRY
P2YR_MELGA     (90)   VLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRY
P2YR_RAT       (101)  VLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRY
Q9Y271         (73)   VCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRC
GPRH_HUMAN     (81)   VLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRF

                      151                                             200
HGPRBMY11      (122)  LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDS---GSEQNGSV
HGPRBMY11v1    (138)  LAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDS---GSEQNGSV
P2Y5_CHICK     (113)  LAIVHPFRSKTLRTKRNARIVCVAVWITVLAGSTPASFFQSTNRQNNTEQ
P2YR_CHICK     (140)  TGVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTI
P2YR_MELGA     (140)  TGVVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTI
P2YR_RAT       (151)  SGVVYPLKSLGRLKKKNAIYVSVLVWLIVVVAISPILFYSGTGIRKNKTV
Q9Y271         (123)  IAIVFPVQNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDEKNNTK
GPRH_HUMAN     (131)  LAIVHPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVV

                      201                                             250
HGPRBMY11      (169)  TSCLE--LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE
HGPRBMY11v1    (185)  TSCLE--LNLYKIAKLQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVE
P2Y5_CHICK     (163)  RTCFENFPESTWKTYLSRIVIFIEIVGFFIPLILNVTCSTMVLRTLNKPL
P2YR_CHICK     (190)  TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKD
P2YR_MELGA     (190)  TCYDT--TADEYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKD
P2YR_RAT       (201)  TCYDS--TSDEYLRSYFIYSMCTTVAMFCIPLVLILGCYGLIVRALIYKD
Q9Y271         (173)  CFEPP--QDNQTKNHVLVLHYVSLFVGFIIPFVIIIVCYTMIILTLLKKS
GPRH_HUMAN     (181)  CLQLY-------REKASHHALVSLAVAFTFPFITTVTCYLLIIRSLRQGL
```

FIG. 6A

```
1    ATGGAGAGAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT   60
1    M  E  R  K  F  M  S  L  Q  P  S  I  S  V  S  E  M  E  P  N     20

61   GGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTT   120
21   G  T  F  S  N  N  N  S  R  N  C  T  I  E  N  F  K  R  E  F     40

121  TTCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA   180
41   F  P  I  V  Y  L  I  I  F  F  W  G  V  L  G  N  G  L  S  I     60

181  TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG   240
61   Y  V  F  L  Q  P  Y  K  K  S  T  S  V  N  V  F  M  L  N  L     80

241  GCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGA   300
81   A  I  S  D  L  L  F  I  S  T  L  P  F  R  A  D  Y  Y  L  R     100

301  GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC   360
101  G  S  N  W  I  F  G  D  L  A  C  R  I  M  S  Y  S  L  Y  V     120

361  AACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATG   420
121  N  M  Y  S  S  I  Y  F  L  T  V  L  S  V  V  R  F  L  A  M     140

421  GTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG   480
141  V  H  P  F  R  L  L  H  V  T  S  I  R  S  A  W  I  L  C  G     160

481  ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG   540
161  I  I  W  I  L  I  M  A  S  S  I  M  L  L  D  S  G  S  E  Q     180

541  AACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC   600
181  N  G  S  V  T  S  C  L  E  L  N  L  Y  K  I  A  K  L  Q  T     200

601  ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT   660
201  M  N  Y  I  A  L  V  V  G  C  L  L  P  F  F  T  L  S  I  C     220

661  TATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT   720
221  Y  L  L  I  I  R  V  L  L  K  V  E  V  P  E  S  G  L  R  V     240

721  TCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTC   780
241  S  H  R  K  A  L  T  T  I  I  I  T  L  I  I  F  F  L  C  F     260

781  CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAA   840
261  L  P  Y  H  T  L  R  T  V  H  L  T  T  W  K  V  G  L  C  K     280

841  GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC   900
281  D  R  L  H  K  A  L  V  I  T  L  A  L  A  A  A  N  A  C  F     300
```

FIG. 2B

```
                       251                                              300
  HGPRBMY11   (217)   VPESGLRVSHRKAFTTIIITLIIFF  FLPYH  RT  L------TTWK
HGPRBMY11v1   (233)   VPESGLRVSHRKAFTTIIITLIIFF  FLPYH  RT  L------TTWK
  P2Y5_CHICK  (213)   ILSRNKLS-KKKVVKMIIVHLVIFCF FMPYN TLI  SLMR--TQTWIN
  P2YR_CHICK  (238)   LDNSPLR---RKSIYSVIIVLTVFAVSYLPFHVV  T  LRARLDFQTPQ
  P2YR_MELGA  (238)   LDNSPLR---RKSIYLVIIVLTVFAVSYLPFHVV  T  LRARLDFQTPQ
    P2YR_RAT  (249)   LDNSPLR---RKSIYLVIIVLTVFAVSYIPFHVV  T  LRARLDFQTPE
      Q9Y271  (221)   MKKNLSS--HKKAIGMIMVVTAAFLVSFMPYHIQRT  LHFLHN--ETKP
  GPRH_HUMAN  (224)   RVEKRLK---TKAVRMIAIVLAIFLVCFVPYHVNRS    LHYR-- HGAS

                       301                                              350
  HGPRBMY11   (261)   GLCKDRLHKALVITLALAAANACFNPLLYYFAG  F   RL SALRKGHP
HGPRBMY11v1   (277)   GLCKDRLHKALVITLALAAANACFNPLLYYFAG  F   RL SALRKGHP
  P2Y5_CHICK  (260)   CSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSDTNS LD --K  --V
  P2YR_CHICK  (285)   CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSR
  P2YR_MELGA  (285)   CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSR
    P2YR_RAT  (296)   CDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKASR
      Q9Y271  (267)   CDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRLS- FRKHSL
  GPRH_HUMAN  (269)   CATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNLLCGKRL

                       351                        379
  HGPRBMY11   (311)   KAK-TKCVFPVSVWLRKETRV--------
HGPRBMY11v1   (327)   KAK-TKCVFPVSVWLRKETRV--------
  P2Y5_CHICK  (306)   QNT--------------------------
  P2YR_CHICK  (335)   SEP-NVQSKSEEMTLNILTEYKQNGDTSL
  P2YR_MELGA  (335)   SEP-NVQSKSEEMTLNILTEYKQNGDTSL
    P2YR_RAT  (346)   SEA-NLQSKSEEMTLNILSEFKQNGDTSL
      Q9Y271  (316)   SVT-YVPRKKASLPEKGEEICKV------
  GPRH_HUMAN  (319)   GPPPSFEGKTNESSLSAKSEL--------
```

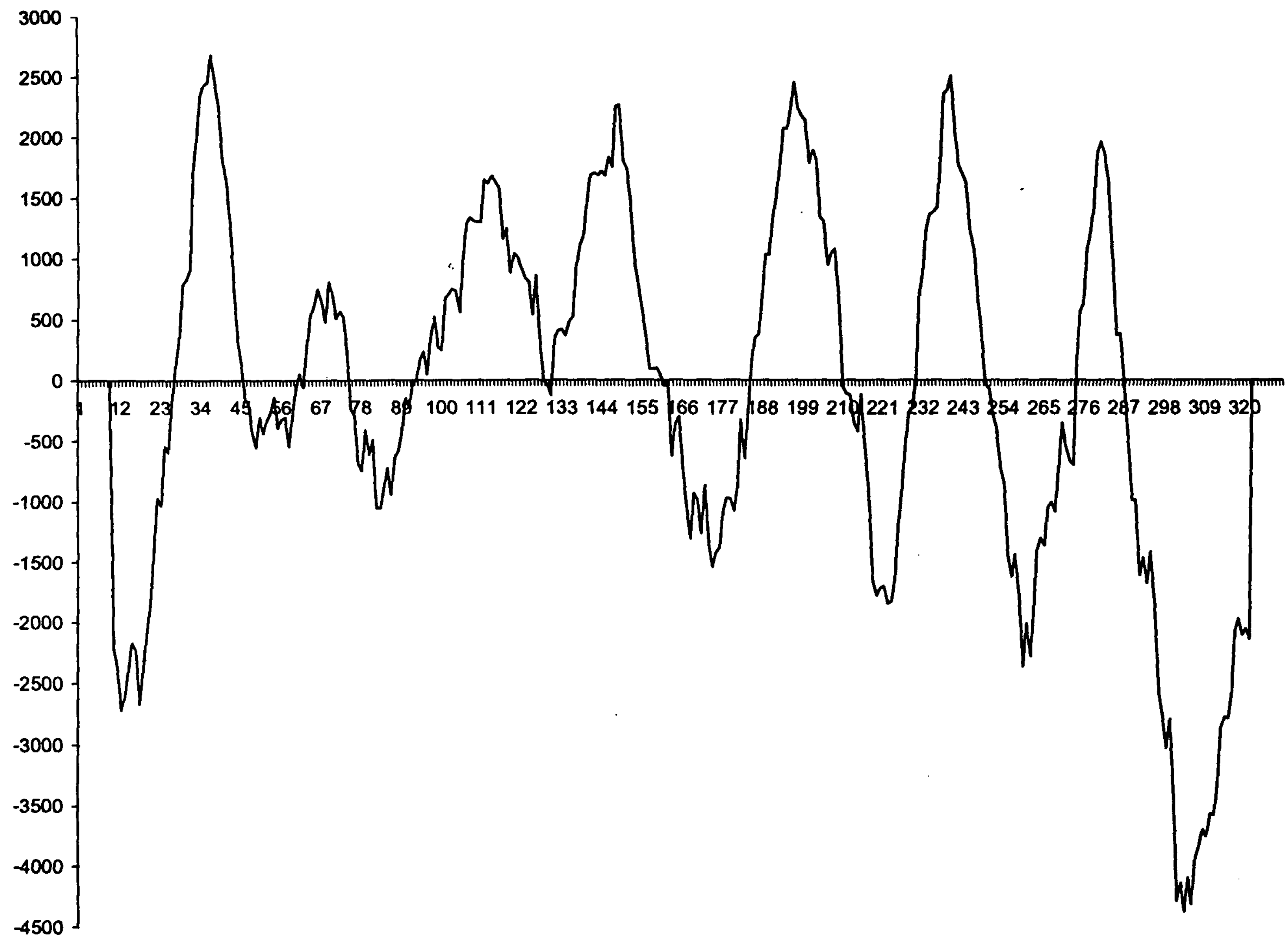

3000
2500
2000
1500
1000
500
0
-500
-1000
-1500
-2000
-2500
-3000
-3500
-4000
-4500
1 12 23 34 45 56 67 78 89 100 111 122 133 144 155 166 177 188 199 210 221 232 243 254 265 276 287 298 309 320

FIG. 3

FIG. 6B

```
 901 AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTC   960
 301 N  P  L  L  Y  Y  F  A  G  E  N  F  K  D  R  L  K  S  A  L    320

 961 AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTG  1020
 321 R  K  G  H  P  Q  K  A  K  T  K  C  V  F  P  V  S  V  W  L    340

1021 AGAAAGGAAACAAGAGTATAA  1041
 341 R  K  E  T  R  V      346
```

FIG. 4

Expression Profiling of Novel Human GPCR, HGPRBMY11

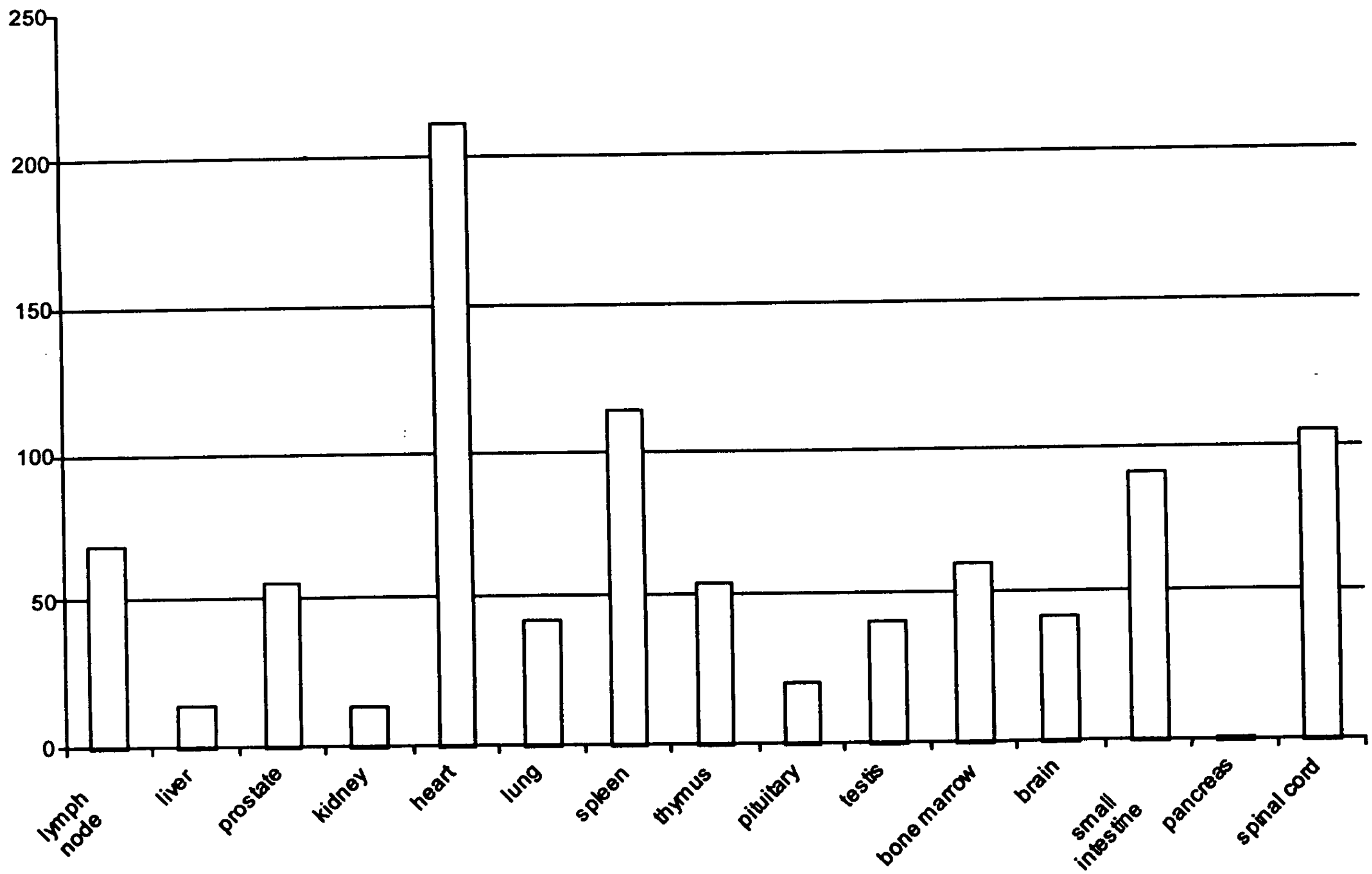


FIG. 5

HGPRBMY11

Protein	Genbank ID	Identities	Similarities
human cysteinyl leukotriene receptor	gi|11422069	37%	49%
chick purinergic receptor 5	gi|P32250	36%	46%
human G-protein-coupled receptor GPR17	gi|Q13304	36%	46%
chick purinergic receptor	gi|P34996	30%	45%
turkey purinergic receptor	gi|P49652	30%	45%
rat purinergic receptor	gi|P49651	30%	44%

HGPRBMY11v1

Protein	Genbank ID	Identities	Similarities
human cysteinyl leukotriene receptor	gi|11422069	37.2%	49%
chick purinergic receptor 5	gi|P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi|Q13304	36.2%	46.1%
chick purinergic receptor	gi|P34996	29.5%	43.9%
turkey purinergic receptor	gi|P49652	29.8%	44.2%
rat purinergic receptor	gi|P49651	29.6%	44%

FIG. 7

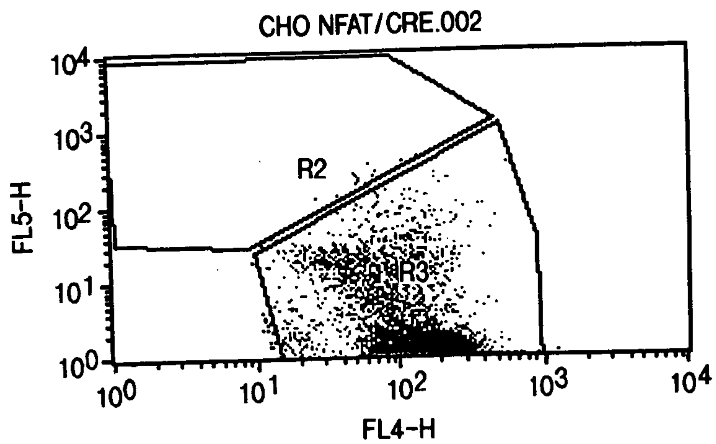

CHO NFAT/CRE.002
R2
R3
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 8

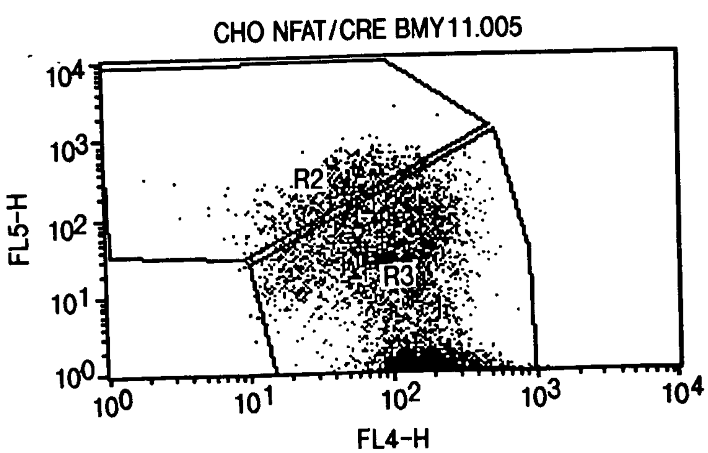

CHO NFAT/CRE BMY11.005
R2
R3
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 9

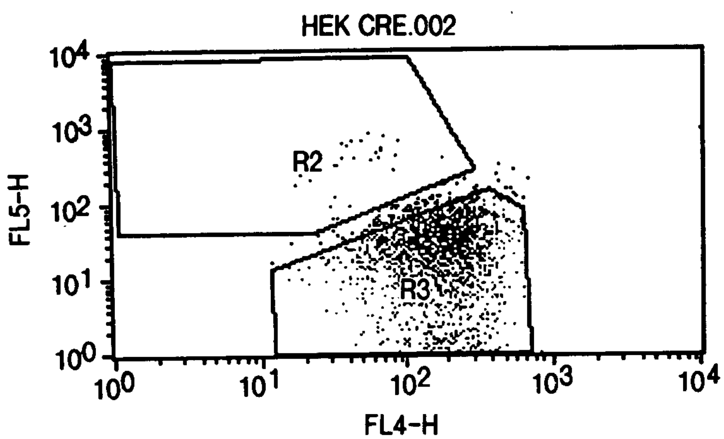

HEK CRE.002
10^4
10^3
10^2
10^1
10^0
FL5-H
R2
R3
10^0
10^1
10^2
10^3
10^4
FL4-H

FIG. 10

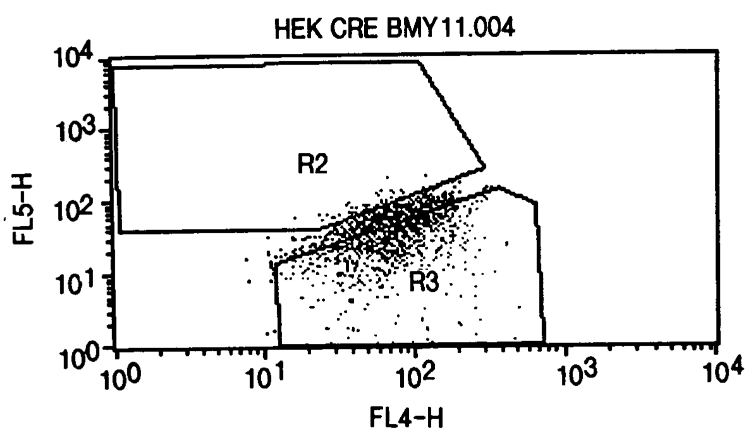
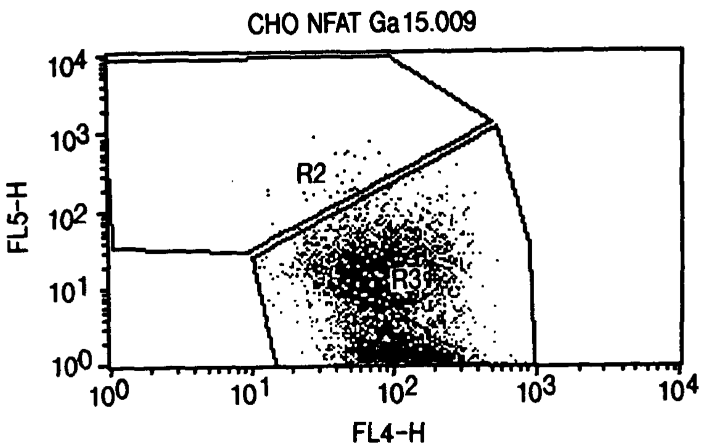
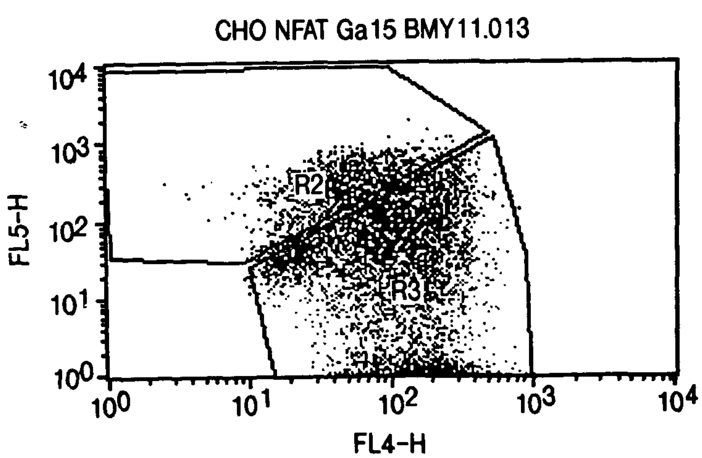

HEK CRE BMY11.004
10^4
10^3
10^2
10^1
10^0
FL5-H
R2
R3
10^0
10^1
10^2
10^3
10^4
FL4-H

FIG. 11



CHO NFAT Ga15.009
10^4
10^3
10^2
10^1
10^0
FL5-H
R2
R3
10^0
10^1
10^2
10^3
10^4
FL4-H

FIG. 12



CHO NFAT Ga15 BMY11.013
10^4
10^3
10^2
10^1
10^0
FL5-H
R2
R3
10^0
10^1
10^2
10^3
10^4
FL4-H

FIG. 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)

Cho NFAT Ga15 BMY11 (Fluorescent vs. Bright Field)

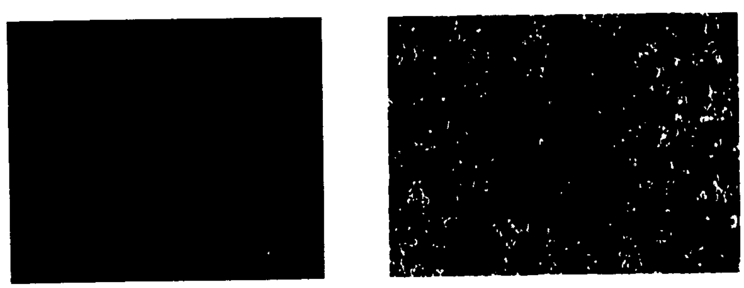


FIG. 14a

Cho-NFAT CRE

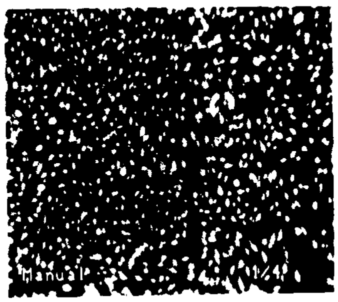


FIG. 14b

Cho-NFAT CRE + F/T/P

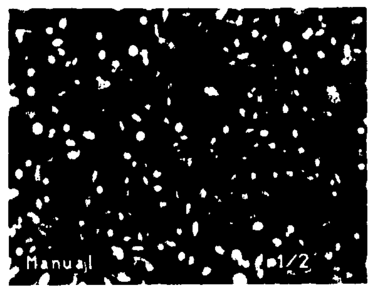


FIG. 14c

Cho-NFAT CRE oGPCR-Intermediate

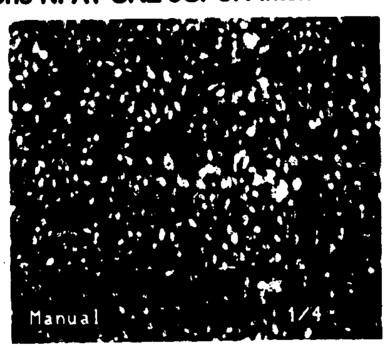


FIG. 14d

Cho-NFAT CRE oGPCR High

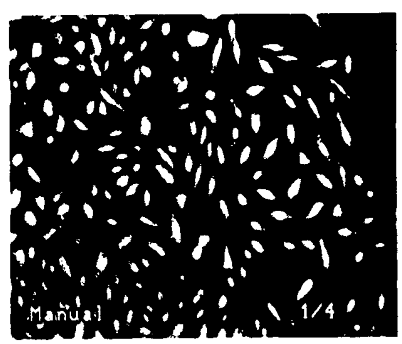


FIG. 15A

```
  1  ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT   60
  1  M  S  L  Q  P  S  I  S  V  S  E  M  E  P  N  G  T  F  S  N    20

 61  AACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAATTTTTCCCAATTGTATAT  120
 21  N  N  S  R  N  C  T  I  E  N  F  K  R  E  F  F  P  I  V  Y    40

121  CTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCCTGCAG  180
 41  L  I  I  F  F  W  G  V  L  G  N  G  L  S  I  Y  V  F  L  Q    60

181  CCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTC  240
 61  P  Y  K  K  S  T  S  V  N  V  F  M  L  N  L  A  I  S  D  L    80

241  CTGTTCATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA  300
 81  L  F  I  S  T  L  P  F  R  A  D  Y  Y  L  R  G  S  N  W  I   100

301  TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGT  360
101  F  G  D  L  A  C  R  I  M  S  Y  S  L  Y  V  N  M  Y  S  S   120

361  ATTTATTTCCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGG  420
121  I  Y  F  L  T  V  L  S  V  V  R  F  L  A  M  V  H  P  F  R   140

421  CTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT  480
141  L  L  H  V  T  S  I  R  S  A  W  I  L  C  G  I  I  W  I  L   160

481  ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCACA  540
161  I  M  A  S  S  I  M  L  L  D  S  G  S  E  Q  N  G  S  V  T   180

541  TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGCC  600
181  S  C  L  E  L  N  L  Y  K  I  A  K  L  Q  T  M  N  Y  I  A   200

601  TTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATT  660
201  L  V  V  G  C  L  L  P  F  F  T  L  S  I  C  Y  L  L  I  I   220

661  CGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA  720
221  R  V  L  L  K  V  E  V  P  E  S  G  L  R  V  S  H  R  K  A   240

721  CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCCTGCCCTATCACACA  780
241  L  T  T  I  I  I  T  L  I  I  F  F  L  C  F  L  P  Y  H  T   260

781  CTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA  840
261  L  R  T  V  H  L  T  T  W  K  V  G  L  C  K  D  R  L  H  K   280

841  GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT  900
281  A  L  V  I  T  L  A  L  A  A  A  N  A  C  F  N  P  L  L  Y   300
```

FIG. 15B

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901  TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA   960
301  Y  F  A  G  E  N  F  K  D  R  L  K  S  A  L  R  K  G  H  P    320

961  CAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAGA   1020
321  Q  K  A  K  T  K  C  V  F  P  V  S  V  W  L  R  K  E  T  R    340

1021 GTATAA  1026
341  V       341
```